> This Raw Listing contains the General Information
> Section and up to first 5 pages.

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 1   <110> APPLICANT: Meyers, Rachel
 2   <120> TITLE OF INVENTION: 21612, 21615, 21620, 21676, 33756, Novel
 3         Human Alcohol Dehydrogenases
 4   <130> FILE REFERENCE: 5800-49
 5   <140> CURRENT APPLICATION NUMBER: US/09/464,039
 6   <141> CURRENT FILING DATE: 1999-12-15
 7   <160> NUMBER OF SEQ ID NOS: 10
 8   <170> SOFTWARE: FastSEQ for Windows Version 3.0
 9   <210> SEQ ID NO 1
10   <211> LENGTH: 260
11   <212> TYPE: PRT
12   <213> ORGANISM: Homo sapiens
13   <400> SEQUENCE: 1
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15          1               5                  10                  15
16         Thr Gly Ala Ser Gly Gly Ile Gly Ala Ala Val Ala Arg Ala Leu Val
17                      20                  25                  30
18         Gln Gln Gly Leu Lys Val Val Gly Cys Ala Arg Thr Val Gly Asn Ile
19                  35                  40                  45
20         Glu Glu Leu Ala Ala Glu Cys Lys Ser Ala Gly Tyr Pro Gly Thr Leu
21              50                  55                  60
22         Ile Pro Tyr Arg Cys Asp Leu Ser Asn Glu Glu Asp Ile Leu Ser Met
23         65                  70                  75                  80
24         Phe Ser Ala Ile Arg Ser Gln His Ser Gly Val Asp Ile Cys Ile Asn
25                          85                  90                  95
26         Asn Ala Gly Leu Ala Arg Pro Asp Thr Leu Leu Ser Gly Ser Thr Ser
27                      100                 105                 110
28         Gly Trp Lys Asp Met Phe Asn Val Asn Val Leu Ala Leu Ser Ile Cys
29                      115                 120                 125
30         Thr Arg Glu Ala Tyr Gln Ser Met Lys Glu Arg Asn Val Asp Asp Gly
31              130                 135                 140
32         His Ile Ile Asn Ile Asn Ser Met Ser Gly His Arg Val Leu Pro Leu
33         145                 150                 155                 160
34         Ser Val Thr His Phe Tyr Ser Ala Thr Lys Tyr Ala Val Thr Ala Leu
35                      165                 170                 175
36         Thr Glu Gly Leu Arg Gln Glu Leu Arg Glu Ala Gln Thr His Ile Arg
37                      180                 185                 190
38         Ala Thr Cys Ile Ser Pro Gly Val Val Glu Thr Gln Phe Ala Phe Lys
39                  195                 200                 205
40         Leu His Asp Lys Asp Pro Glu Lys Ala Ala Ala Thr Tyr Glu Gln Met
41              210                 215                 220
42         Lys Cys Leu Lys Pro Glu Asp Val Ala Glu Ala Val Ile Tyr Val Leu
43         225                 230                 235                 240
44         Ser Thr Pro Ala His Ile Gln Ile Gly Asp Ile Gln Met Arg Pro Thr
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ENTERED

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45                         245                250                255
46          Glu Gln Val Thr
47                         260
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49     <211> LENGTH: 1909
50     <212> TYPE: DNA
51     <213> ORGANISM: Homo sapiens
52     <220> FEATURE:
53     <221> NAME/KEY: misc_feature
54     <222> LOCATION: (0)...(0)
55     <223> OTHER INFORMATION: 21620 ADH
56     <220> FEATURE:
57     <221> NAME/KEY: CDS
58     <222> LOCATION: (421)...(1203)
59     <221> NAME/KEY: misc_feature
60     <222> LOCATION: (1)...(1909)
61     <223> OTHER INFORMATION: n = A,T,C or G
62     <400> SEQUENCE: 2
63          tacttagact cagccggctt ttccacgctt tgcctgaccc tgctttgctc aactgtacgt      60
64          cttgtttcgt tttctgttct gcgccgttac agatccaagc tctgaaaaac cagaaagtta     120
65          actggtaagt ttagtctttt tgtctttttat ttcaggtccc ggatccggtg atccaaatct     180
66          aagaactgct cctcagtgag tgttgccttt acttctaggc ctgtacggaa gtgttacttc     240
67          tgctctaaaa gctgcggaat tctaatacga ctcactatag ggagtcgacc cacgcgtccg     300
68          gggtctaggc gcggatcgga cccaagcagg tcggcggcgg cggcaggaga gcggccgggc     360
69          gtcagctcct cgacccccgt gtcgggctag tccagcgagg cggacgggcg gcgtgggccc     420
70          atg gcc agg ccc ggc atg gag cgg tgg cgc gac cgg ctg gcg ctg gtg      468
71          Met Ala Arg Pro Gly Met Glu Arg Trp Arg Asp Arg Leu Ala Leu Val
72           1               5                  10                  15
73          acg ggg gcc tcg ggg ggc atc ggc gcg gcc gtg gcc cgg gcc ctg gtc      516
74          Thr Gly Ala Ser Gly Gly Ile Gly Ala Ala Val Ala Arg Ala Leu Val
75                          20                  25                  30
76          cag cag gga ctg aag gtg gtg ggc tgc gcc cgc act gtg ggc aac atc      564
77          Gln Gln Gly Leu Lys Val Val Gly Cys Ala Arg Thr Val Gly Asn Ile
78                          35                  40                  45
79          gag gag ctg gct gct gaa tgt aag agt gca ggc tac ccc ggg act ttg      612
80          Glu Glu Leu Ala Ala Glu Cys Lys Ser Ala Gly Tyr Pro Gly Thr Leu
81                          50                  55                  60
82          atc ccc tac aga tgt gac cta tca aat gaa gag gac atc ctc tcc atg      660
83          Ile Pro Tyr Arg Cys Asp Leu Ser Asn Glu Glu Asp Ile Leu Ser Met
84           65                  70                  75                  80
85          ttc tca gct atc cgt tct cag cac agc ggt gta gac atc tgc atc aac      708
86          Phe Ser Ala Ile Arg Ser Gln His Ser Gly Val Asp Ile Cys Ile Asn
87                          85                  90                  95
88          aat gct ggc ttg gcc cgg cct gac acc ctg ctc tca ggc agc acc agt      756
89          Asn Ala Gly Leu Ala Arg Pro Asp Thr Leu Leu Ser Gly Ser Thr Ser
90                          100                 105                 110
91          ggt tgg aag gac atg ttc aat gtg aac gtg ctg gcc ctc agc atc tgc      804
92          Gly Trp Lys Asp Met Phe Asn Val Asn Val Leu Ala Leu Ser Ile Cys
93                          115                 120                 125
94          aca cgg gaa gcc tac cag tcc atg aag gag cgg aat gtg gac gat ggg      852
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        95          Thr Arg Glu Ala Tyr Gln Ser Met Lys Glu Arg Asn Val Asp Asp Gly
        96              130                 135                 140
        97          cac atc att aac atc aat agc atg tct ggc cac cga gtg tta ccc ctg      900
        98          His Ile Ile Asn Ile Asn Ser Met Ser Gly His Arg Val Leu Pro Leu
        99          145                 150                 155                 160
       100          tct gtg acc cac ttc tat agt gcc acc aag tat gcc gtc act gcg ctg      948
       101          Ser Val Thr His Phe Tyr Ser Ala Thr Lys Tyr Ala Val Thr Ala Leu
       102                          165                 170                 175
       103          aca gag gga ctg agg caa gag ctt cgg gag gcc cag acc cac atc cga      996
       104          Thr Glu Gly Leu Arg Gln Glu Leu Arg Glu Ala Gln Thr His Ile Arg
       105                          180                 185                 190
       106          gcc acg tgc atc tct cca ggt gtg gtg gag aca caa ttc gcc ttc aaa     1044
       107          Ala Thr Cys Ile Ser Pro Gly Val Val Glu Thr Gln Phe Ala Phe Lys
       108                          195                 200                 205
       109          ctc cac gac aag gac cct gag aag gca gct gcc acc tat gag caa atg     1092
       110          Leu His Asp Lys Asp Pro Glu Lys Ala Ala Ala Thr Tyr Glu Gln Met
       111                          210                 215                 220
       112          aag tgt ctc aaa ccc gag gat gtg gcc gag gct gtt atc tac gtc ctc     1140
       113          Lys Cys Leu Lys Pro Glu Asp Val Ala Glu Ala Val Ile Tyr Val Leu
       114          225                 230                 235                 240
       115          agc act ccc gca cac atc cag att gga gac atc cag atg agg ccc acg     1188
       116          Ser Thr Pro Ala His Ile Gln Ile Gly Asp Ile Gln Met Arg Pro Thr
       117                          245                 250                 255
       118          gag cag gtg acc tag tgactgtggg agctcctcct tccctcccca cccttcatgg     1243
W-->   119          Glu Gln Val Thr
       120                          260
       121          cttgcctcct gcctctggat tttaggtgtt gatttctgga tcacgggata ccacttcctg     1303
       122          tccacacccc gaccagggc tagaaaattt gtttgagatt tttatatcat cttgtcaaat     1363
       123          tgcttcagtt gtaaatgtga aaaatgggct ggggaaagga ggtggtgtcc ctaattgttt     1423
       124          tacttgttaa cttgttcttg tgccctggg cacttggcct ttgtctgctc tcagtgtctt     1483
       125          ccctttgaca tgggaaagga gttgtggcca aaatccccat cttcttgcac ctcaacgtct     1543
W-->   126          gtggctyang ggctggggtg gcagagggag gccttcacct tatatctgtg ttgttatcca     1603
       127          gggctccaga cttcctcctc tgcctgcccc actgcaccct ctccccctta tctatctcct     1663
       128          tctcggctcc ccagcccagt cttggcttct tgtccccctcc tggggtcatc cctccactct     1723
       129          gactctgact atggcagcag aacaccaggg cctggcccag tggatttcat ggtgatcatt     1783
       130          aaaaaagaaa aatcgcaacc aaaaaaaaaa aaaaagggc gggccgctag actagtytag     1843
W-->   131          agaaaaaacc tcccacacct ccccybdamm ytkacgccgn acgcnanggg ggcaatcaag     1903
       132          gacgct                                                                1909
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       134   <211> LENGTH: 260
       135   <212> TYPE: PRT
       136   <213> ORGANISM: Homo sapiens
       137   <400> SEQUENCE: 3
       138          Met Glu Lys Cys Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu
       139          1                   5                   10                  15
       140          Asn His His Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser
       141                          20                  25                  30
       142          Ile Arg Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Arg Val Asp
       143                          35                  40                  45
       144          Ile Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
```

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145              50                    55                    60
146        Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His Phe
147        65                    70                    75                    80
148        Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala Pro Ser
149                          85                    90                    95
150        Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly His Ile Asp
151                          100                   105                   110
152        Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn Thr Lys Ala Ala
153                     115                   120                   125
154        Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe Thr Lys Glu Leu Ser
155             130                   135                   140
156        Arg Arg Leu Gln Gly Ser Gly Val Thr Val Asn Ala Leu His Pro Gly
157        145                   150                   155                   160
158        Val Ala Arg Thr Glu Leu Gly Arg His Thr Gly Ile His Gly Ser Thr
159                          165                   170                   175
160        Phe Ser Ser Thr Thr Leu Gly Pro Ile Phe Trp Leu Leu Val Lys Ser
161                          180                   185                   190
162        Pro Glu Leu Ala Ala Gln Pro Ser Thr Tyr Leu Ala Val Ala Glu Glu
163                     195                   200                   205
164        Leu Ala Asp Val Ser Gly Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala
165             210                   215                   220
166        Pro Ala Pro Glu Ala Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala
167        225                   230                   235                   240
168        Glu Ser Ala Arg Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln
169                          245                   250                   255
170        Pro Leu Pro Arg
171                          260
172   <210> SEQ ID NO 4
173   <211> LENGTH: 1153
174   <212> TYPE: DNA
175   <213> ORGANISM: Homo sapiens
176   <220> FEATURE:
177   <221> NAME/KEY: misc_feature
178   <222> LOCATION: (0)...(0)
179   <223> OTHER INFORMATION: 33756 ADH
180   <220> FEATURE:
181   <221> NAME/KEY: CDS
182   <222> LOCATION: (265)...(1047)
183   <221> NAME/KEY: misc_feature
184   <222> LOCATION: (1)...(1153)
185   <223> OTHER INFORMATION: n = A,T,C or G
186   <400> SEQUENCE: 4
187        ccgcgccccg ccctcgcagc ccanntncgg acgcgggccc agccgcgcct gcgcttccgc      60
188        tcgcctgtgg ctgcaannag cgcgctcttc ctcggagcta cccaggcggc tggtgtagca     120
189        gcaagctccg cgccgacccc tgacgcctga cgcctgtccc cggcccggca tgagccgcta     180
190        cctgctgccg ctgtcggcgc tgggcacggt agcaggcgct cgccgtgctg ctcaagaggc     240
191        aacatcatcc tggcctgccg agac atg gag aag tgt gag gcg gca gca aag         291
192                                    Met Glu Lys Cys Glu Ala Ala Ala Lys
193                                     1                   5
194        gac atc cgc ggg gag acc ctc aat cac cat gtc aac gcc cgg cac ctg       339
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(W--> markers appear at lines 187 and 188)

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195            Asp Ile Arg Gly Glu Thr Leu Asn His His Val Asn Ala Arg His Leu
196             10              15              20                  25
197            gac ttg gct tcc ctc aag tct atc cga gag ttt gca gca aag atc att    387
198            Asp Leu Ala Ser Leu Lys Ser Ile Arg Glu Phe Ala Ala Lys Ile Ile
199                            30              35                  40
200            gaa gag gag gag cga gtg gac att cta atc aac aac gcg ggt gtg atg    435
201            Glu Glu Glu Glu Arg Val Asp Ile Leu Ile Asn Asn Ala Gly Val Met
202                            45              50                  55
203            cgg tgc ccc cac tgg acc acc gag gac ggc ttc gag atg cag ttt ggc    483
204            Arg Cys Pro His Trp Thr Thr Glu Asp Gly Phe Glu Met Gln Phe Gly
205                        60              65                  70
206            gtt aac cac ctg ggt cac ttt ctc ttg aca aac ttg ctg ctg gac aag    531
207            Val Asn His Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys
208                75              80              85
209            ctg aaa gcc tca gcc cct tcg cgg atc atc aac ctc tcg tcc ctg gcc    579
210            Leu Lys Ala Ser Ala Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala
211             90              95              100                 105
212            cat gtt gct ggg cac ata gac ttt gac gac ttg aac tgg cag acg agg    627
213            His Val Ala Gly His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg
214                            110             115                 120
215            aag tat aac acc aaa gcc gcc tac tgc cag agc aag ctc gcc atc gtc    675
216            Lys Tyr Asn Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val
217                        125             130                 135
218            ctc ttc acc aag gag ttg agc cgg cgg ctg caa ggc tct ggt gtg act    723
219            Leu Phe Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr
220                        140             145                 150
221            gtc aac gcc ctg cac ccc ggc gtg gcc agg aca gag ctg ggc aga cac    771
222            Val Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His
223                155             160                 165
224            acg ggc atc cat ggc tcc acc ttc tcc agc acc aca ctc ggg ccc atc    819
225            Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro Ile
226            170             175                 180                 185
227            ttc tgg ctg ctg gtc aag agc ccc gag ctg gcc gcc cag ccc agc aca    867
228            Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro Ser Thr
229                        190             195                 200
230            tac ctg gcc gtg gcg gag gaa ctg gcg gat gtt tcc gga aag tac ttc    915
231            Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly Lys Tyr Phe
232                        205             210                 215
233            gat gga ctc aaa cag aag gcc ccg gcc ccc gag gct gag gat gag gag    963
234            Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala Glu Asp Glu Glu
235                        220             225                 230
236            gtg gcc cgg agg ctt tgg gct gaa agt gcc cgc ctg gtg ggc tta gag    1011
237            Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg Leu Val Gly Leu Glu
238                235             240                 245
239            gct ccc tct gtg agg gag cag ccc ctc ccc aga taa cctctggagc         1057
W-->    240    Ala Pro Ser Val Arg Glu Gln Pro Leu Pro Arg
241                250             255                 260
242            agatttgaaa gccaggatgg cgcctccaga ccgaggacag ctgtccgcca tgcccgcagc  1117
243            ttcctggcac tacctgagcc gggagaccca ggactg                            1153
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                    <210> SEQ ID NO 5

Line	?	Error/Warning	Original Text
119	W	Line data has been corrected	Glu Gln Val Thr *
126	W	"N" or "Xaa" used: Feature required	gtggctyang ggctggggtg gcagagggag gccttcac
131	W	"N" or "Xaa" used: Feature required	agaaaaaacc tcccacacct ccccybdamm ytkacgcc
187	W	"N" or "Xaa" used: Feature required	ccgcgccccg ccctcgcagc ccanntncgg acgcgggc
188	W	"N" or "Xaa" used: Feature required	tcgcctgtgg ctgcaannag cgcgctcttc ctcggagc
240	W	Line data has been corrected	Ala Pro Ser Val Arg Glu Gln Pro Leu Pro A
306	W	"N" or "Xaa" used: Feature required	gcntgtgggt cccttcttna aattgggtcc ccccgttt
307	W	"N" or "Xaa" used: Feature required	gttcaaagac nggncctttt gtcgggggct ccttgaag
308	W	"N" or "Xaa" used: Feature required	gctttttttt ttgggggncc ccccctttg ggaacccc
378	W	Line data has been corrected	Pro Ser Val Arg Glu Gln Pro Leu Pro Arg
457	W	"N" or "Xaa" used: Feature required	aactccgccc atcccgcccc taactccgnc ccagttcc
547	W	Line data has been corrected	Lys Leu Glu Lys Leu Met Asn Gln Met Asn A
610	W	"N" or "Xaa" used: Feature required	atgcaaaagc cgagnccgcc tcggcctcta agctattc
666	W	Line data has been corrected	Tyr Val Thr Gly Asn Pro Val Ile Ile Asp G

● **CORRECTION SUMMARY** ●
PATENT APPLICATION **US/09/464,039**

Input Set: **I464039.RAW**

Line	Original Text	Corrected Data
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119	Glu Gln Val Thr *	Glu Gln Val Thr
240	Ala Pro Ser Val Arg Glu Gln Pro Leu Pro A	Ala Pro Ser Val Arg Glu Gln Pro Leu Pro A
378	Pro Ser Val Arg Glu Gln Pro Leu Pro Arg	Pro Ser Val Arg Glu Gln Pro Leu Pro Arg
547	Lys Leu Glu Lys Leu Met Asn Gln Met Asn A	Lys Leu Glu Lys Leu Met Asn Gln Met Asn A
666	Tyr Val Thr Gly Asn Pro Val Ile Ile Asp G	Tyr Val Thr Gly Asn Pro Val Ile Ile Asp G